

SEQUENCE LISTING

<110> MOULAND, Andrew J.
 COHEN, Eric A.
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 LUO, Ming
 DUCHAINE, Thomas



<120> MAMMALIAN STAUFEN AND USE THEREOF

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<170> PatentIn Ver. 2.1

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Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala
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Met Ser Gln
1

gtt caa gtg caa gtt cag aac cca tct gct gct ctc tca ggg agc caa 465
Val Gln Val Gln Val Gln Asn Pro Ser Ala Ala Leu Ser Gly Ser Gln
5 10 15

ata ctg aac aag aac cag tct ctt ctc tca cag cct ttg atg agt att 513

Ile	Leu	Asn	Lys	Asn	Gln	Ser	Leu	Leu	Ser	Gln	Pro	Leu	Met	Ser	Ile	
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cct tct act act agc tct ctg ccc tct gaa aat gca ggt aga ccc att															561	
Pro	Ser	Thr	Thr	Ser	Ser	Leu	Pro	Ser	Glu	Asn	Ala	Gly	Arg	Pro	Ile	
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45															50	
caa	aac	tct	gct	tta	ccc	tct	gca	tct	att	aca	tcc	acc	agt	gca	gct	609
Gln	Asn	Ser	Ala	Leu	Pro	Ser	Ala	Ser	Ile	Thr	Ser	Thr	Ser	Ala	Ala	
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gca	gaa	agc	ata	acc	cct	act	gta	gaa	cta	aat	gca	ctg	tgc	atg	aaa	657
Ala	Glu	Ser	Ile	Thr	Pro	Thr	Val	Glu	Leu	Asn	Ala	Leu	Cys	Met	Lys	
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75															80	
ctt	gga	aaa	aaa	cca	atg	tat	aag	cct	gtt	gac	cct	tac	tct	cgg	atg	705
Leu	Gly	Lys	Lys	Pro	Met	Tyr	Lys	Pro	Val	Asp	Pro	Tyr	Ser	Arg	Met	
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Gln	Ser	Thr	Tyr	Asn	Tyr	Asn	Met	Arg	Gly	Gly	Ala	Tyr	Pro	Pro	Arg	
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Tyr	Phe	Tyr	Pro	Phe	Pro	Val	Pro	Pro	Leu	Leu	Tyr	Gln	Val	Glu	Leu	
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125															130	
tct	gtg	gga	gga	cag	caa	ttt	aat	ggc	aaa	gga	aag	aca	aga	cag	gct	849
Ser	Val	Gly	Gly	Gln	Gln	Phe	Asn	Gly	Lys	Gly	Lys	Thr	Arg	Gln	Ala	
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Ala	Lys	His	Asp	Ala	Ala	Lys	Ala	Leu	Arg	Ile	Leu	Gln	Asn	Glu		
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Pro	Leu	Pro	Glu	Arg	Leu	Glu	Val	Asn	Gly	Arg	Glu	Ser	Glu	Glu	Glu	
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170															175	
aat	ctc	aat	aaa	tct	gaa	ata	agt	caa	gtg	ttt	gag	att	gca	ctt	aaa	993
Asn	Leu	Asn	Lys	Ser	Glu	Ile	Ser	Gln	Val	Phe	Glu	Ile	Ala	Leu	Lys	
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cgg	aac	ttg	cct	gtg	aat	ttc	gag	gtg	gcc	cg	gag	agt	ggc	cca	ccc	1041
Arg	Asn	Leu	Pro	Val	Asn	Phe	Glu	Val	Ala	Arg	Glu	Ser	Gly	Pro	Pro	
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205															210	
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His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe Val Gly			
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gaa ggt gaa ggg aaa agc aag aag att tca aag aaa aat gcc gcc ata			1137
Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala Ile			
230	235	240	
gct gtt ctt gag gag ctg aag aag tta ccg ccc ctg cct gca gtt gaa			1185
Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala Val Glu			
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cga gta aag cct aga atc aaa aag aaa aca aaa ccc ata gtc aag cca			1233
Arg Val Lys Pro Arg Ile Lys Lys Thr Lys Pro Ile Val Lys Pro			
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cag aca agc cca gaa tat ggc cag ggg atc aat ccg att agc cga ctg			1281
Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser Arg Leu			
280	285	290	
gcc cag atc cag cag gca aaa aag gag aag gag cca gag tac acg ctc			1329
Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr Thr Leu			
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ctc aca gag cga ggc ctc ccg cgc cgc agg gag ttt gtg atg cag gtg			1377
Leu Thr Glu Arg Gly Leu Pro Arg Arg Glu Phe Val Met Gln Val			
310	315	320	
aag gtt gga aac cac act gca gaa gga acg ggc acc aac aag aag gtg			1425
Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys Lys Val			
325	330	335	
gcc aag cgc aat gca gcc gag aac atg ctg gag atc ctt ggt ttc aaa			1473
Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly Phe Lys			
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gtc ccg cag cgg cag ccc acc aaa ccc gca ctc aag tca gag gag aag			1521
Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu Glu Lys			
360	365	370	
aca ccc ata aag aaa cca ggg gat gga aga aaa gta acc ttt ttt gaa			1569
Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe Phe Glu			
375	380	385	
cct ggc tct ggg gat gaa aat ggg act agt aat aaa gag gat gag ttc			1617
Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp Glu Phe			
390	395	400	
agg atg cct tat cta agt cat cag cag ctg cct gct gga att ctt ccc			1665

Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile Leu Pro
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atg gtg ccc gag gtc gcc cag gct gta gga gtt agt caa gga cat cac 1713
Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly His His
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acc aaa gat ttt acc agg gca gct ccg aat cct gcc aag gcc acg gta 1761
Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala Thr Val
440 445 450

act gcc atg ata gcc cga gag ttg ttg tat ggg ggc acc tcg ccc aca 1809
Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser Pro Thr
455 460 465

gcc gag acc att tta aag aat aac atc tct tca ggc cac gta ccc cat 1857
Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val Pro His
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520 525 530

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535 540 545

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565 570 575

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Met Ser Ile Pro Ser Thr Thr Ser Ser Leu Pro Ser Glu Asn Ala Gly
35 40 45

Arg Pro Ile Gln Asn Ser Ala Leu Pro Ser Ala Ser Ile Thr Ser Thr
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Ser Ala Ala Ala Glu Ser Ile Thr Pro Thr Val Glu Leu Asn Ala Leu
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Cys Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr
85 90 95

Ser Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr
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Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln
115 120 125

Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr
130 135 140

Arg Gln Ala Ala Lys His Asp Ala Ala Ala Lys Ala Leu Arg Ile Leu
145 150 155 160

Gln Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser
165 170 175

Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile
180 185 190

Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser
195 200 205

Gly Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu
210 215 220

Phe Val Gly Glu Gly Glu Gly Lys Ser Lys Lys Ile Ser Lys Lys Asn
225 230 235 240

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245 250 255

Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile
260 265 270

Val Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile
275 280 285

Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu
290 295 300

Tyr Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe Val
305 310 315 320

Met Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Thr Asn
325 330 335

Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu
340 345 350

Gly Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser
355 360 365

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370 375 380

Phe Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu
385 390 395 400

Asp Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly
405 410 415

Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln
420 425 430

Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys
435 440 445

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450 455 460

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465 470 475 480

Val Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu
485 490 495

Ser Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn
500 505 510

Asn Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro
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Leu Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met
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Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val

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10

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Asp	Pro	Tyr	Ser	Arg	Met	Gln	Ser	Thr	Tyr	Asn	Tyr	Asn	Met	Arg	Gly	
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Gly	Ala	Tyr	Pro	Pro	Arg	Tyr	Phe	Tyr	Pro	Phe	Pro	Val	Pro	Pro	Leu	
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Leu	Tyr	Gln	Val	Glu	Leu	Ser	Val	Gly	Gly	Gln	Gln	Phe	Asn	Gly	Lys	
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Gly	Lys	Thr	Arg	Gln	Ala	Ala	Lys	His	Asp	Ala	Ala	Lys	Ala	Leu		
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Phe	Glu	Ile	Ala	Leu	Lys	Arg	Asn	Leu	Pro	Val	Asn	Phe	Glu	Val	Ala	
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Arg	Glu	Ser	Gly	Pro	Pro	His	Met	Lys	Asn	Phe	Val	Thr	Lys	Val	Ser	
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Val	Gly	Glu	Phe	Val	Gly	Glu	Gly	Gly	Ser	Lys	Lys	Ile	Ser			
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aag aaa aat gcc gcc ata gct gtt ctt gag gag ctg aag aag tta ccg															1009	
Lys	Lys	Asn	Ala	Ala	Ile	Ala	Val	Leu	Glu	Leu	Lys	Lys	Leu	Pro		
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Pro	Leu	Pro	Ala	Val	Glu	Arg	Val	Lys	Pro	Arg	Ile	Lys	Lys	Thr		
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Lys	Pro	Ile	Val	Lys	Pro	Gln	Thr	Ser	Pro	Glu	Tyr	Gly	Gln	Ile		
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Asn Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys			
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Glu Pro Glu Tyr Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg			
225	230	235	
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Glu Phe Val Met Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr			
240	245	250	
ggc acc aac aag aag gtg gcc aag cgc aat gca gcc gag aac atg ctg			1297
Gly Thr Asn Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu			
255	260	265	
gag atc ctt ggt ttc aaa gtc ccg cag cgg cag ccc acc aaa ccc gca			1345
Glu Ile Leu Gly Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala			
270	275	280	
ctc aag tca gag gag aag aca ccc ata aag aaa cca ggg gat gga aga			1393
Leu Lys Ser Glu Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg			
285	290	295	300
aaa gta acc ttt ttt gaa cct ggc tct ggg gat gaa aat ggg act agt			1441
Lys Val Thr Phe Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser			
305	310	315	
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Asn Lys Glu Asp Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu			
320	325	330	
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Pro Ala Gly Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly			
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Val Ser Gln Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn			
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Pro Ala Lys Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr			
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Gly Gly Thr Ser Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser			
385	390	395	
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Ser Gly His Val Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu
400 405 410

gac tat ctt tcc aga gtc cag gga ttc cag gtt gaa tac aaa gac ttc 1777
Asp Tyr Leu Ser Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe
415 420 425

ccc aaa aac aac aag aac gaa ttt gta tct ctt atc aat tgc tcc tct 1825
Pro Lys Asn Asn Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser
430 435 440

cag cca cct ctg atc agc cat ggt atc ggc aag gat gtg gag tcc tgc 1873
Gln Pro Pro Leu Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys
445 450 455 460

cat gat atg gct gcg ctg aac atc tta aag ttg ctg tct gag ttg gac 1921
His Asp Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp
465 470 475

caa caa agt aca gag atg cca aga aca gga aac gga cca atg tct gtg 1969
Gln Gln Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val
480 485 490

tgt ggg agg tgc tgaacctttt ctggccatga accattataa aatcccaaca 2021
Cys Gly Arg Cys
495

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tgtatctata catatggctc ttgaggactt agcttcact acactacagg atatgatctc 3041
catgttagtcc atataaacct gcagagtat tttccagagt gctcgatact gtttaattaca 3101
tctccatttag ggctgaaaag aatgacctac gtttctgtat acagctgtgt tgcttttgg 3161
gttgtgttac tgtacacaga agtgtgtgca ctgaggctct gcgtgtggtc cgtatggaaa 3221
acctggtagc cctgcgagtt aagtactgct tccattcatt gtttacgctg gaattttct 3281
ccccatggaa tctaagtaaa acttaagtgt ttgtcatcaa taaatggtaa tactaaaaaa 3341
aaaaaaaaa 3348

<210> 8
<211> 496
<212> PRT
<213> Homo sapiens

<400> 8
Met Lys Leu Gly Lys Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser
1 5 10 15
Arg Met Gln Ser Thr Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro
20 25 30
Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu Leu Tyr Gln Val
35 40 45
Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg
50 55 60
Gln Ala Ala Lys His Asp Ala Ala Lys Ala Leu Arg Ile Leu Gln
65 70 75 80
Asn Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly Arg Glu Ser Glu

	85	90	95
Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val Phe Glu Ile Ala	100	105	110
Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala Arg Glu Ser Gly	115	120	125
Pro Pro His Met Lys Asn Phe Val Thr Lys Val Ser Val Gly Glu Phe	130	135	140
Val Gly Glu Gly Glu Lys Ser Lys Lys Ile Ser Lys Lys Asn Ala	145	150	155
Ala Ile Ala Val Leu Glu Glu Leu Lys Lys Leu Pro Pro Leu Pro Ala	165	170	175
Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys Thr Lys Pro Ile Val	180	185	190
Lys Pro Gln Thr Ser Pro Glu Tyr Gly Gln Gly Ile Asn Pro Ile Ser	195	200	205
Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu Pro Glu Tyr	210	215	220
Thr Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Glu Phe Val Met	225	230	235
Gln Val Lys Val Gly Asn His Thr Ala Glu Gly Thr Gly Thr Asn Lys	245	250	255
Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile Leu Gly	260	265	270
Phe Lys Val Pro Gln Arg Gln Pro Thr Lys Pro Ala Leu Lys Ser Glu	275	280	285
Glu Lys Thr Pro Ile Lys Lys Pro Gly Asp Gly Arg Lys Val Thr Phe	290	295	300
Phe Glu Pro Gly Ser Gly Asp Glu Asn Gly Thr Ser Asn Lys Glu Asp	305	310	315
Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala Gly Ile	325	330	335
Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser Gln Gly			

340	345	350
His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala Lys Ala		
355	360	365
Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly Thr Ser		
370	375	380
Pro Thr Ala Glu Thr Ile Leu Lys Asn Asn Ile Ser Ser Gly His Val		
385	390	395
Pro His Gly Pro Leu Thr Arg Pro Ser Glu Gln Leu Asp Tyr Leu Ser		
405	410	415
Arg Val Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys Asn Asn		
420	425	430
Lys Asn Glu Phe Val Ser Leu Ile Asn Cys Ser Ser Gln Pro Pro Leu		
435	440	445
Ile Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp Met Ala		
450	455	460
Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln Ser Thr		
465	470	475
Glu Met Pro Arg Thr Gly Asn Gly Pro Met Ser Val Cys Gly Arg Cys		
485	490	495

<210> 9
 <211> 2857
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (3)..(1784)

<220>
 <221> CDS
 <222> (324)..(1784)

<400> 9
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 Gly Ala Ala Pro Pro Pro Ser Leu Pro Ala Arg Leu Arg Ala Pro
 1 5 10 15

agc cgc tct tca gcg ttt gcg ctg gct gtc gtc gcg tct gtg tgc gct	95		
Ser Arg Ser Ser Ala Phe Ala Leu Ala Val Val Ala Ser Val Cys Ala			
20	25	30	
ccc cct tct tct gag ccc cgg cct ggc ggc gcc cgc ctt cgc ctc cgc	143		
Pro Pro Ser Ser Glu Pro Arg Pro Gly Gly Ala Arg Leu Arg Leu Arg			
35	40	45	
cac tcc gcc tct tcc ctc ctc tgg tcg gcc cct ttt tcc tcg ccg tct	191		
His Ser Ala Ser Ser Leu Leu Trp Ser Ala Pro Phe Ser Ser Pro Ser			
50	55	60	
tca ctt gct tct tca cct cct cgc cgc cca aga ccg ccg gcc ccg	239		
Ser Leu Ala Ser Ser Pro Pro Arg Arg Pro Arg Pro Pro Ala Pro			
65	70	75	
gga cga gct ctg ggg aag cag cca gaa agt ata gct tct acc att gag	287		
Gly Arg Ala Leu Gly Lys Gln Pro Glu Ser Ile Ala Ser Thr Ile Glu			
80	85	90	95
ctc aat gca ctg tgt gtg aaa ctg gaa aga aaa cca atg tat aag ccc	335		
Leu Asn Ala Leu Cys Val Lys Leu Glu Arg Lys Pro Met Tyr Lys Pro			
100	105	110	
gtg gac cct cac tct cgg atg cag tcc acc tac agc tat ggc atg cgt	383		
Val Asp Pro His Ser Arg Met Gln Ser Thr Tyr Ser Tyr Gly Met Arg			
115	120	125	
gga ggt gcc tat ccc ccc aga tac ttt tac cca ttt cca gtc cca cct	431		
Gly Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro			
130	135	140	
tta ctc tac caa gtt gag ctc tcc gtg ggc gga cag cag ttt aat ggg	479		
Leu Leu Tyr Gln Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly			
145	150	155	
aaa gga aag atg aga cca ccc gtg aaa cac gat gcc cct gcc cgt gcg	527		
Lys Gly Lys Met Arg Pro Pro Val Lys His Asp Ala Pro Ala Arg Ala			
160	165	170	175
ctg agg act ctg cag agt gaa ccc ctg cca gaa agg ttg gag gta aat	575		
Leu Arg Thr Leu Gln Ser Glu Pro Leu Pro Glu Arg Leu Glu Val Asn			
180	185	190	
gga aga gaa gca gag gaa gaa aac ctc aat aaa tcg gaa ata agc caa	623		
Gly Arg Glu Ala Glu Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln			
195	200	205	

gtg ttt gaa att gcg ctg aag cgg aat ttg cct gtg aat ttt gag gtg	671		
Val Phe Glu Ile Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val			
210	215	220	
gcc cgg gag agt ggc cca cca cac atg aag aac ttt gtg acc agg gtt	719		
Ala Arg Glu Ser Gly Pro Pro His Met Lys Asn Phe Val Thr Arg Val			
225	230	235	
tca gtt ggg gaa ttt gta ggg gaa gga gaa ggg aaa agc aag aag atc	767		
Ser Val Gly Glu Phe Val Gly Glu Gly Lys Ser Lys Lys Ile			
240	245	250	255
tcc aag aag aat gcg gcc agg gct gtt ctg gag cag ctt agg agg ctg	815		
Ser Lys Lys Asn Ala Ala Arg Ala Val Leu Glu Gln Leu Arg Arg Leu			
260	265	270	
cca ccc ctc cct gct gtg gag cga gtg aag ccc aga atc aag aag aaa	863		
Pro Pro Leu Pro Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Lys			
275	280	285	
agt cag ccc acc tgc aag aca gcc ccg gat tat ggc caa ggg atg aat	911		
Ser Gln Pro Thr Cys Lys Thr Ala Pro Asp Tyr Gly Gln Gly Met Asn			
290	295	300	
cct att agt aga ctt gca cag atc cag cag gca aaa aag gag aag gag	959		
Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Glu			
305	310	315	
cca gag tac atg ctc ctt aca gaa cga ggt ctt cca cgt cgc agg gag	1007		
Pro Glu Tyr Met Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu			
320	325	330	335
ttt gtg atg cag gta aag gtt ggg cat cac act gca gaa gga gtg ggt	1055		
Phe Val Met Gln Val Lys Val Gly His His Thr Ala Glu Gly Val Gly			
340	345	350	
acc aat aag aag gtg gcc aag cgt aat gct gct gag aac atg ctg gag	1103		
Thr Asn Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu			
355	360	365	
atc ctg ggg ttc aaa gtt ccc cag gcg cag cct gcc aag cca gca ctc	1151		
Ile Leu Gly Phe Lys Val Pro Gln Ala Gln Pro Ala Lys Pro Ala Leu			
370	375	380	
aaa tca gaa gag aag act cca gta aag aaa cca gga gac gga agg aaa	1199		
Lys Ser Glu Glu Lys Thr Pro Val Lys Lys Pro Gly Asp Gly Arg Lys			
385	390	395	

gta acg ttt ttt gaa cct agc cct ggg gat gaa aat gga act agt aac	1247		
Val Thr Phe Phe Glu Pro Ser Pro Gly Asp Glu Asn Gly Thr Ser Asn			
400	405	410	415
 aag gac gag gag ttc agg atg cct tat ctt agc cat cag cag ctg cca	1295		
Lys Asp Glu Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro			
420	425	430	
 gct gga att ctc ccc atg gtg ccg gaa gtt gcc cag gct gtc ggg gtt	1343		
Ala Gly Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val			
435	440	445	
 agt caa gga cac cac acc aaa gat ttc acc agg gca gct cca aat cct	1391		
Ser Gln Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro			
450	455	460	
 gcc aag gca acg gta act gcc atg ata gcc cga gag ttg ttg tac ggg	1439		
Ala Lys Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly			
465	470	475	
 ggc acc tcg ccc aca gcc gag acc att tta aag agt aac atc tct tca	1487		
Gly Thr Ser Pro Thr Ala Glu Thr Ile Leu Lys Ser Asn Ile Ser Ser			
480	485	490	495
 ggc cac gta ccc cat gga cct cgc act aga ccc tct gag caa ctg tac	1535		
Gly His Val Pro His Gly Pro Arg Thr Arg Pro Ser Glu Gln Leu Tyr			
500	505	510	
 tac ctt tcc aga gcc cag gga ttc cag gtt gaa tac aaa gat ttt ccc	1583		
Tyr Leu Ser Arg Ala Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro			
515	520	525	
 aag aac aac aag aac gag tgt gta tct ctc atc aac tgc tcc tca cag	1631		
Lys Asn Asn Lys Asn Glu Cys Val Ser Leu Ile Asn Cys Ser Ser Gln			
530	535	540	
 ccg cct ctc gtc agt cat ggc atc ggc aag gat gtg gag tcc tgt cat	1679		
Pro Pro Leu Val Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His			
545	550	555	
 gat atg gct gca ctg aac att tta aag ctg ctg tct gag ttg gac caa	1727		
Asp Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln			
560	565	570	575
 cag agc aca gag atg cca aga aca gga aat gga cca gtt tca gcg tgc	1775		
Gln Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Val Ser Ala Cys			
580	585	590	

ggg agg tgc tgaacctttt ctggccacaa accattataa aacccaacat 1824
Gly Arg Cys

atataactgaa aataactgaga actgcttga aaatttggaa tatctgataa ctccagtggg 1884
ccaagacatg gtggataaaaa atgtggcaaa gacgacaaga aacttcaggt ggtagccctg 1944
gttgtgctgg cggtctgtga ttagtgcgtg ctctgccatc catccagaca gaaaccagcc 2004
ccaacgcctc cagttctgtt tttgcattgt gacaaagaga gcacagccaa ttctcatgct 2064
ggcttcttca gatactttga aaaacccgga cagccacacc agagaggct tatagcgcc 2124
ccggagctaa acggaccaga gaaaaggcca gtgcttccta ctgcacatga ctgactcagc 2184
tccgccacac gtagcaccac tgtaaccact gctttctttt cagtttcatt tttttctttt 2244
gattgataca acactataat tttcatttca gttccttagt cgtgtctact taccttagcag 2304
tttagaaact gtcagtcatg taactggcaa ggatcacagc ccgggtgggt ggcattctgt 2364
gcctctggct tggctgaaca gttctggaat taccaccaga atccttgact ccctgcccct 2424
tgtataaaatt ggacagctta ggactttaa actttagatc aaaagatatg gtcctttta 2484
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cctgtaggcc cagaagacta caggctggtg tccctagagg gcccaataca gtcaattcca 2664
acctctaagt cggggaaagg tgacaggttt cctggtgctg gtgtgcacag gggcaggcag 2724
gtcagctggc ctggggaaaga gcattgtggc tccttagtgcg gccctgcttc cactcttgg 2784
ttagctggaa ccttcccact catgaaat aagtaaactc actttctttt tcaccaataa 2844
atggtaatac taa 2857

<210> 10
<211> 594
<212> PRT
<213> Mus musculus

<400> 10
Gly Ala Ala Pro Pro Pro Ser Leu Pro Ala Arg Leu Arg Ala Pro Ser

1	5	10	15
Arg Ser Ser Ala Phe Ala Leu Ala Val Val Ala Ser Val Cys Ala Pro			
20	25	30	
Pro Ser Ser Glu Pro Arg Pro Gly Gly Ala Arg Leu Arg Leu Arg His			
35	40	45	
Ser Ala Ser Ser Leu Leu Trp Ser Ala Pro Phe Ser Ser Pro Ser Ser			
50	55	60	
Leu Ala Ser Ser Pro Pro Arg Arg Arg Pro Arg Pro Pro Ala Pro Gly			
65	70	75	80
Arg Ala Leu Gly Lys Gln Pro Glu Ser Ile Ala Ser Thr Ile Glu Leu			
85	90	95	
Asn Ala Leu Cys Val Lys Leu Glu Arg Lys Pro Met Tyr Lys Pro Val			
100	105	110	
Asp Pro His Ser Arg Met Gln Ser Thr Tyr Ser Tyr Gly Met Arg Gly			
115	120	125	
Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr Pro Phe Pro Val Pro Pro Leu			
130	135	140	
Leu Tyr Gln Val Glu Leu Ser Val Gly Gly Gln Gln Phe Asn Gly Lys			
145	150	155	160
Gly Lys Met Arg Pro Pro Val Lys His Asp Ala Pro Ala Arg Ala Leu			
165	170	175	
Arg Thr Leu Gln Ser Glu Pro Leu Pro Glu Arg Leu Glu Val Asn Gly			
180	185	190	
Arg Glu Ala Glu Glu Asn Leu Asn Lys Ser Glu Ile Ser Gln Val			
195	200	205	
Phe Glu Ile Ala Leu Lys Arg Asn Leu Pro Val Asn Phe Glu Val Ala			
210	215	220	
Arg Glu Ser Gly Pro Pro His Met Lys Asn Phe Val Thr Arg Val Ser			
225	230	235	240
Val Gly Glu Phe Val Gly Glu Gly Lys Ser Lys Lys Ile Ser			
245	250	255	
Lys Lys Asn Ala Ala Arg Ala Val Leu Glu Gln Leu Arg Arg Leu Pro			
260	265	270	
Pro Leu Pro Ala Val Glu Arg Val Lys Pro Arg Ile Lys Lys Ser			
275	280	285	
Gln Pro Thr Cys Lys Thr Ala Pro Asp Tyr Gly Gln Gly Met Asn Pro			
290	295	300	
Ile Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys Lys Glu Lys Pro			
305	310	315	320
Glu Tyr Met Leu Leu Thr Glu Arg Gly Leu Pro Arg Arg Arg Glu Phe			
325	330	335	
Val Met Gln Val Lys Val Gly His His Thr Ala Glu Gly Val Gly Thr			
340	345	350	
Asn Lys Lys Val Ala Lys Arg Asn Ala Ala Glu Asn Met Leu Glu Ile			
355	360	365	
Leu Gly Phe Lys Val Pro Gln Ala Gln Pro Ala Lys Pro Ala Leu Lys			
370	375	380	
Ser Glu Glu Lys Thr Pro Val Lys Lys Pro Gly Asp Gly Arg Lys Val			

385	390	395	400
Thr Phe Phe Glu Pro Ser Pro Gly Asp Glu Asn Gly Thr Ser Asn Lys			
405	410	415	
Asp Glu Glu Phe Arg Met Pro Tyr Leu Ser His Gln Gln Leu Pro Ala			
420	425	430	
Gly Ile Leu Pro Met Val Pro Glu Val Ala Gln Ala Val Gly Val Ser			
435	440	445	
Gln Gly His His Thr Lys Asp Phe Thr Arg Ala Ala Pro Asn Pro Ala			
450	455	460	
Lys Ala Thr Val Thr Ala Met Ile Ala Arg Glu Leu Leu Tyr Gly Gly			
465	470	475	480
Thr Ser Pro Thr Ala Glu Thr Ile Leu Lys Ser Asn Ile Ser Ser Gly			
485	490	495	
His Val Pro His Gly Pro Arg Thr Arg Pro Ser Glu Gln Leu Tyr Tyr			
500	505	510	
Leu Ser Arg Ala Gln Gly Phe Gln Val Glu Tyr Lys Asp Phe Pro Lys			
515	520	525	
Asn Asn Lys Asn Glu Cys Val Ser Leu Ile Asn Cys Ser Ser Gln Pro			
530	535	540	
Pro Leu Val Ser His Gly Ile Gly Lys Asp Val Glu Ser Cys His Asp			
545	550	555	560
Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser Glu Leu Asp Gln Gln			
565	570	575	
Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro Val Ser Ala Cys Gly			
580	585	590	
Arg Cys			

<210> 11
 <211> 487
 <212> PRT
 <213> Mus musculus

<400> 11			
Met Tyr Lys Pro Val Asp Pro His Ser Arg Met Gln Ser Thr Tyr Ser			
1	5	10	15
Tyr Gly Met Arg Gly Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr Pro Phe			
20	25	30	
Pro Val Pro Pro Leu Leu Tyr Gln Val Glu Leu Ser Val Gly Gly Gln			
35	40	45	
Gln Phe Asn Gly Lys Gly Lys Met Arg Pro Pro Val Lys His Asp Ala			
50	55	60	
Pro Ala Arg Ala Leu Arg Thr Leu Gln Ser Glu Pro Leu Pro Glu Arg			
65	70	75	80
Leu Glu Val Asn Gly Arg Glu Ala Glu Glu Asn Leu Asn Lys Ser			
85	90	95	
Glu Ile Ser Gln Val Phe Glu Ile Ala Leu Lys Arg Asn Leu Pro Val			
100	105	110	

Asn Phe Glu Val Ala Arg Glu Ser Gly Pro Pro His Met Lys Asn Phe
115 120 125
Val Thr Arg Val Ser Val Gly Glu Phe Val Gly Glu Gly Glu Lys
130 135 140
Ser Lys Lys Ile Ser Lys Lys Asn Ala Ala Arg Ala Val Leu Glu Gln
145 150 155 160
Leu Arg Arg Leu Pro Pro Leu Pro Ala Val Glu Arg Val Lys Pro Arg
165 170 175
Ile Lys Lys Ser Gln Pro Thr Cys Lys Thr Ala Pro Asp Tyr Gly
180 185 190
Gln Gly Met Asn Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln Ala Lys
195 200 205
Lys Glu Lys Glu Pro Glu Tyr Met Leu Leu Thr Glu Arg Gly Leu Pro
210 215 220
Arg Arg Arg Glu Phe Val Met Gln Val Lys Val Gly His His Thr Ala
225 230 235 240
Glu Gly Val Gly Thr Asn Lys Lys Val Ala Lys Arg Asn Ala Ala Glu
245 250 255
Asn Met Leu Glu Ile Leu Gly Phe Lys Val Pro Gln Ala Gln Pro Ala
260 265 270
Lys Pro Ala Leu Lys Ser Glu Glu Lys Thr Pro Val Lys Lys Pro Gly
275 280 285
Asp Gly Arg Lys Val Thr Phe Phe Glu Pro Ser Pro Gly Asp Glu Asn
290 295 300
Gly Thr Ser Asn Lys Asp Glu Glu Phe Arg Met Pro Tyr Leu Ser His
305 310 315 320
Gln Gln Leu Pro Ala Gly Ile Leu Pro Met Val Pro Glu Val Ala Gln
325 330 335
Ala Val Gly Val Ser Gln Gly His His Thr Lys Asp Phe Thr Arg Ala
340 345 350
Ala Pro Asn Pro Ala Lys Ala Thr Val Thr Ala Met Ile Ala Arg Glu
355 360 365
Leu Leu Tyr Gly Gly Thr Ser Pro Thr Ala Glu Thr Ile Leu Lys Ser
370 375 380
Asn Ile Ser Ser Gly His Val Pro His Gly Pro Arg Thr Arg Pro Ser
385 390 395 400
Glu Gln Leu Tyr Tyr Leu Ser Arg Ala Gln Gly Phe Gln Val Glu Tyr
405 410 415
Lys Asp Phe Pro Lys Asn Asn Lys Asn Glu Cys Val Ser Leu Ile Asn
420 425 430
Cys Ser Ser Gln Pro Pro Leu Val Ser His Gly Ile Gly Lys Asp Val
435 440 445
Glu Ser Cys His Asp Met Ala Ala Leu Asn Ile Leu Lys Leu Leu Ser
450 455 460
Glu Leu Asp Gln Gln Ser Thr Glu Met Pro Arg Thr Gly Asn Gly Pro
465 470 475 480
Val Ser Ala Cys Gly Arg Cys
485

<210> 12
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
 oligonucleotide

<400> 12
agcttaatta gctgac 16

<210> 13
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
 oligonucleotide

<400> 13
agctgtcagc taatta 16

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
 oligonucleotide

<400> 14
cctggatccg aaagtatagc ttctaccatt g 31

<210> 15
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 15
tacataagct tctagatggc cagaaaaggc tcagca

36

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 16
ggatgaatcc tattagtaga cttgcac

27

<210> 17
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 17
gctctagatt caaagttccc caggcgcag

29

<210> 18
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 18
tttaagcttc tcagagggtc tagtgcgag

29

<210> 19
<211> 22

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<400> 19
caatgtataa gcccgtggac cc          22

<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<400> 20
aaaaagcttg tgcaagtcta ctaataggat tcatcc          36

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<400> 21
atagcccgag agttgttg          18

<210> 22
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oligonucleotide

<400> 22
tacataagct tctagatggc cagaaaaggt tcagca          36
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<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 23
tacatgtcga cttcctgccc ggctgcggg 29

<210> 24
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 24
tacaatcttag attatcagcg gccgcacctc ccacacacag acat 44

<210> 25
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 25
tacataagct taagccacca tggtcaaagt tccccaggcg c 41

<210> 26
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

oligonucleotide

<400> 26

tacaatctag agcggccgcg ctcagagggt ctagtgcgag

40

<210> 27

<211> 705

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

oligonucleotide

<400> 27

Met Gln Ala Val Phe Glu Thr Thr Leu Thr Gln Lys Met Asp Gly Val
1 5 10 15

Met Ile Val Gln Glu Thr Thr Asp Leu Ala Asp Thr Leu Glu Asn
20 25 30

Ala Ser Ile Ser Ala Glu Lys Ser Glu Gln Lys Pro Glu Arg Leu His
35 40 45

Pro Gln His Trp Cys Gly Gln His Lys Phe Glu Ala Asp Ser Pro Thr
50 55 60

Asn Phe Tyr Asp Tyr Thr Asn Ala Lys Glu Lys Glu Lys Ser Ala Met
65 70 75 80

Cys Arg Val Ala Glu Ile Ala Arg Phe Asn Lys Leu Arg His Val Tyr
85 90 95

Asn Leu Gln Asp Glu Ser Gly Pro Ala His Lys Lys Leu Phe Thr Val
100 105 110

Lys Leu Val Leu Thr Glu Ala Glu Thr Phe Glu Gly Ser Gly Thr Ser
115 120 125

Ile Lys Arg Ala Gln Gln Ala Ser Ala Glu Ala Ala Leu Lys Gly Thr
130 135 140

Lys Leu Pro Leu Pro Thr Glu Lys Pro Thr Lys Lys Arg Ile Asn Asp
145 150 155 160

Thr Thr Lys Pro His Arg Val Leu Gln Asn Val Cys Arg Thr Leu Gln
165 170 175

Tyr Gln Met Pro Asn Tyr Ile Ser Cys Asn Pro Pro Val Tyr Pro Asp
180 185 190

Pro Gly Cys Pro Leu Pro Glu His Ile Leu Leu Pro Leu Glu Ser Met
195 200 205

Ala Leu Tyr Ala Pro Pro Phe Pro Thr Leu Pro Ile Asp Pro Ala Arg
210 215 220

Pro Gln Gly Pro Lys Leu Gln Ala Val Ile Val Asn Ile Asn Gly Lys
225 230 235 240

Ser Ile Ala Thr Gly Ile Gly Glu Thr Tyr Pro Leu Ala Lys Gln Asp
245 250 255

Ala Ala Ala Lys Ala Leu Ala Val Leu Ser Pro Leu Leu Arg Glu His
260 265 270

Gln Asn Gly Ser Asp Asn Gly Phe Gly Lys Glu Asn Ile Pro Val His
275 280 285

Lys Gln Lys Ser Val Ile Ser Asp Ile His Glu Lys Ala Tyr Gln Leu
290 295 300

Lys Val Asn Val Val Phe Glu Val Leu Lys Glu Glu Gly Pro Pro His
305 310 315 320

Asp Arg Gln Tyr Val Val Arg Cys Ala Phe Val Thr Ser Gly Asn Val
325 330 335

Val Lys Ala Glu Ala Val Gly Lys Gly Lys Lys Lys Ser Ala Gln
340 345 350

Gln Glu Ala Cys Thr Gln Leu Leu Ala Thr Val Glu His Leu Thr Pro
355 360 365

Glu Asn Asn Pro Val Ala Leu Ala Thr Asn Val Cys Lys Thr Gln Lys
370 375 380

Lys Leu Ala Ala Met Asn Arg Glu Pro Lys Arg Lys Thr Ile Val Lys
385 390 395 400

Asp Lys Lys Met Asp Pro Leu Tyr Gly His Gln Ile Asn Pro Val Ser
405 410 415

Arg Leu Ile Gln Val Thr Gln Ala Lys Ser Lys Glu His Pro Thr Phe
420 425 430

Glu Leu Val Ala Glu His Gly Val Ser Lys Tyr Lys Glu Phe Ile Ile
435 440 445

Gln Val Lys Tyr Gly Asp Asp Val Gln Glu Gly Lys Gly Pro Asn Lys
450 455 460

Arg Leu Ala Lys Arg Ala Ala Ala Glu Ala Met Leu Glu Ser Ile Gly
465 470 475 480

Phe Val Lys Pro Leu Pro Pro Gly Lys Ser Leu Leu Lys Lys Met
485 490 495

Ile Asp Cys Asp Pro Ser Leu Pro Glu Ile Ser His Trp Thr Gly Pro
500 505 510

Pro Pro Thr Ala Val Ser Val Ser Thr Ser Glu Pro Asp Thr Ser Glu
515 520 525

Ala Ala Gln Leu Ser Pro Glu Gln Thr Asp Ile Ser Glu Lys Arg Glu
530 535 540

Leu Ser Pro Asp Thr Glu Lys Arg Arg Val Thr Phe Asn Ser Gln Val
545 550 555 560

His Ala Cys Pro Pro Pro Gly Asp Gln Asp Tyr Pro Asn Ser Ile Val
565 570 575

Gln Ser Leu Lys Lys Asp Ala Ile Val Glu Gly Lys Ile Arg Arg Leu
580 585 590

Lys Arg Ser Lys Glu Asn Arg Arg Ala Leu Thr Ala Glu Gln Ile Val
595 600 605

Glu Leu Ser Glu Arg Ala Gln Ser Tyr Leu Gln Thr Lys Asn Thr Thr
610 615 620

Ile Gln Ser Ser Gln Ser Ser Ala His His His Leu Glu Gln Leu
625 630 635 640

Ser Asp Phe Phe Lys Phe Ser Leu Gln Tyr Thr Ser Phe Pro Gln Val
645 650 655

Gly Ile Asp Gln His Phe Thr Ile Val Ser Ile Gly Leu Glu Ala Pro
660 665 670

Leu Val Gly His Gly Thr Gly Cys Ser Thr Thr Glu Ala Asp Glu Asn
675 680 685

Ala Ala Leu Asp Ala Ile Ala Lys Leu Lys Glu Leu Ser Ala Ser Lys
690 695 700

Thr

705